

SEQUENCE LISTING

<110> Lukyanov, Sergey
 Fradkov, Arcady
 Labas, Yulii
 Matz, Mikhail
 Lukyanov, Konstantin
 Gurskaya, Nadezda

<120> FAR RED SHIFTED FLUORESCENT PROTEINS

<130> CLON-028WO

<140> Unassigned

<141> 2001-10-12

<150> 60/240,018

<151> 2000-10-12

<150> 60,306,131

<151> 2001-07-16

<160> 28

<170> FastSEQ for Windows Version 4.0

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<211> 910

<212> DNA

<213> heteractis crispa

<400> 1

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ccatttacag gtacgcagag catgaggatt catgtcaccc aaggggctcc attaccattt 240
gccttcgaca ttttggcacc gtgttgtgag tacggcagca ggacctttgt ccaccatacg 300
gcagagattc ccgatttctt caagcagtc ttcctgaag gctttacttg ggaaagaacc 360
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tgcttatat acaaggtgaa agtccttggt accaattttc ctgctgatgg ccccgatgatg 480
aagaacaaat caggaggatg ggagccatgc actgaggtgg tttatccaga gaatggtgtc 540
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tatacttctt acaggtccaa gaaagcagtc cgtgccttga caatgccagg atttcatttt 660
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<210> 2

<211> 227

<212> PRT

<213> heteractis crispa

<400> 2

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Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Cys Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

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 <212> DNA
 <213> heteractis crispa

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 ggaaggcacg gttaatggcc attatttcaa gtgtgaagga gagggagacg gcaaccatt 180
 tacaggtagc cagagcatga ggattcatgt caccgaagg gctccattac catttgcctt 240
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 caaatcagaa ggatgggagc catgcactga ggtggtttat ccagataatg gtgtcctgtg 540
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 ctgctgtcag ctttttggtta aagcccgaag gacaaaagga cattttagt tttagtttat 840
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<210> 4
 <211> 227
 <212> PRT
 <213> heteractis crispa

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 20 25 30

09976673-101201

Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
35 40 45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
50 55 60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65 70 75 80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
85 90 95
Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
100 105 110
Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
115 120 125
Asp Gly Pro Val Met Lys Asn Lys Ser Glu Gly Trp Glu Pro Cys Thr
130 135 140
Glu Val Val Tyr Pro Asp Asn Gly Val Leu Cys Gly Arg Asn Val Met
145 150 155 160
Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
165 170 175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180 185 190
Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
195 200 205
Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
210 215 220
Lys Ala Asn
225

<210> 5
<211> 684
<212> DNA
<213> heteractis crispa

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atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat tttggcaccg 180
tgttgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
aagcagtctt tccctgaagg ctttacttgg gagggaact gccttatata caaggtgaaa 360
attcttactg ctcatcagga cacaagcctg gagggaact gccttatata caaggtgaaa 360
gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaacaatc aggaggtgg 420
gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
gcccttaaag tcggtgatcg tcgtttgatc tgccatctct ataactctta caggtccaag 540
aaagcagtcg gtgccttgac aatgccagga ttcatcttta cagacatccg ctttcagatg 600
ccgaggaaaa cgaaagacga gtactttgaa ctgtacgaag catctgtggc taggtacagt 660
gatcttctcg aaaaagcaaa ttga 684

<210> 6
<211> 227
<212> PRT
<213> heteractis crispa

<400> 6
Met Ala Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met Glu
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Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
20 25 30
Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
35 40 45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
50 55 60

Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

<210> 7
 <211> 681
 <212> DNA
 <213> heteractis crispa

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 aggatcatg tcaccgaagg ggctccatta ccatttgctt tcgacatttt ggcaccgtgt 180
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 cttggtacca attttccctgc tgatggcccc gtgatgaaga acaaatacagg aggatgggag 420
 ccaagcactg aggtgggtta tccagagaat ggtgtcctgt gtggacgtaa tgtgatggcc 480
 cttaaagtcg gtgatcgtcg tttgatctgc catcactata cttcttacag gtccaagaaa 540
 gcagtcgctg ccttgacaat gccaggattt cattttacag acatccgcct tcagatgctg 600
 aggaaagaga aagacgagta ctttgaactg tacgaagcat ctgtggctag gtacagtgat 660
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<210> 8
 <211> 226
 <212> PRT
 <213> heteractis crispa

<400> 8
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 20 25 30
 Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly Ala
 35 40 45
 Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr Gly
 50 55 60
 Ser Arg Thr Phe Val His Thr Ala Glu Ile Pro Asp Phe Phe Lys
 65 70 75 80
 Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95

Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly	Asn
			100					105					110		
Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro	Ala	Asp
		115					120					125			
Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser	Thr	Glu
	130					135					140				
Val	Val	Tyr	Pro	Glu	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val	Met	Ala
145					150					155					160
Leu	Lys	Val	Gly	Asp	Arg	Arg	Leu	Ile	Cys	His	His	Tyr	Thr	Ser	Tyr
			165					170						175	
Arg	Ser	Lys	Lys	Ala	Val	Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe	His	Phe
		180						185					190		
Thr	Asp	Ile	Arg	Leu	Gln	Met	Leu	Arg	Lys	Glu	Lys	Asp	Glu	Tyr	Phe
	195					200						205			
Glu	Leu	Tyr	Glu	Ala	Ser	Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro	Glu	Lys
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Ala	Asn														
225															

<210> 9
 <211> 681
 <212> DNA
 <213> heteractis crispa

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 aggattcatg tcaccgaagg ggctccatta ccatttgcct tcgacatttt ggccaccgtg 180
 tgtgcgtacg gcagcaggac ctttgtccac catacggcag agattcccga tttcttcaag 240
 cagtctttcc ctgaaggctt tacttgggaa agaaccacaa cctatgaaga tggaggcatt 300
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 cttggtacca attttcctgc tgatggcccc gtgatgaaga acaaatacagg aggatgggag 420
 ccaagcactg aggtgggttta tccagagaat ggtgtcctgt gtggacgtaa tgtgatggcc 480
 cttaaagtcg gtgatcgtcg tttgatctgc catcactata cttcttacag gtccaagaaa 540
 gcagtcctgt ccttgacaat gccaggattt cattttacag acatccgcct tcagatgctg 600
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 cttcctgaaa aagcaaattg a 681

<210> 10
 <211> 226
 <212> PRT
 <213> heteractis crispa

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 Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly Ala
 35 40 45
 Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Ala Tyr Gly
 50 55 60
 Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe Lys
 65 70 75 80
 Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95
 Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly Asn
 100 105 110
 Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala Asp
 115 120 125

Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu
 130 135 140
 Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met Ala
 145 150 155 160
 Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser Tyr
 165 170 175
 Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His Phe
 180 185 190
 Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe
 195 200 205
 Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys
 210 215 220
 Ala Asn
 225

<210> 11
 <211> 687
 <212> DNA
 <213> heteractis crispa

<400> 11
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 agcatgagaa tccacgtgac cgagggcgcc cccctgccct tcgccttcga catcctggcc 180
 ccctgctgcg agtacggcag caggaccttc gtgcaccaca ccgccgagat ccccgacttc 240
 ttcaagcaga gcttccccga gggcttcacc tgggagagaa ccaccaccta cgaggacggc 300
 ggcatacctga ccgccaccca ggacaccagc ctggagggca actgcctgat ctacaagggtg 360
 aaggtgcacg gcaccaactt ccccgccgac ggccccgtga tgaagaacaa gagcggcgccg 420
 tgggagccca gcaccgaggt ggtgtacccc gagaacggcg tgctgtgctg ccggaacgtg 480
 atggccctga aggtggggcga ccggcacctg atctgccacc actacaccag ctaccggagc 540
 aagaaggccg tgccgcgcct gaccatgccc ggcttccact tcaccgacat ccggtccag 600
 atgctgctga agaagaagga cgagtacttc gagctgtacg aggccagcgt ggccccgtac 660
 agcgacctgc ccgagaaggc caactga 687

<210> 12
 <211> 227
 <212> PRT
 <213> heteractis crispa

<400> 12
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 20 25 30
 Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val His Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160

Ala Leu Lys Val Gly Asp Arg His Leu Ile Cys His His Tyr Thr Ser
165 170 175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180 185 190
Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Thr Lys Asp Glu Tyr
195 200 205
Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
210 215 220
Lys Ala Asn
225

<210> 13
<211> 687
<212> DNA
<213> heteractis crispa

<400> 13
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aacggccact acttcaagtg cgagggcgag ggcgacggca accccttcgc cggcaccag 120
agcatgcgga tccacgtgac cgagggcgcc cccctgccct tcgccttcga catcctggcc 180
ccctgctgcy agtacggcag caggaccttc gtgcaccaca ccgccgagat ccccgacttc 240
ttcaagcaga gcttccccga gggcttcacc tgggagagaa ccaccaccta cgaggacggc 300
ggcatcctga cgcgccacca ggacaccagc ctggagggca actgcctgat ctacaagggtg 360
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tgggagccca gcaccgaggt ggtgtacccc gagaacggcg tgctgtgcgg ccggaacgtg 480
atggccctga aggtgggcca ccggcggtg atctgccacc actacaccag ctaccggagc 540
aagaaggccg tgcgggccct gaccatgcc ggcttcact tcaccgacat ccggctgcag 600
atgctgcgga aggagaagga cgagtacttc gagctgtacg aggccagcgt ggcccgggtac 660
agcgacctgc ccgagaaggc caactga 687

<210> 14
<211> 227
<212> PRT
<213> heteractis crispa

<400> 14
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Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
35 40 45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
50 55 60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65 70 75 80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
85 90 95
Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
100 105 110
Asn Cys Leu Ile Tyr Lys Val Lys Val His Gly Thr Asn Phe Pro Ala
115 120 125
Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
130 135 140
Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
145 150 155 160
Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser
165 170 175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180 185 190

Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

<210> 15
 <211> 1396
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 15
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 gcgcggcacc cagagcatgc ggatccacgt gaccgagggc gccccctgc ccttcgcctt 180
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 gatccccgac ttcttcaagc agagcttccc cgagggcttc acctgggaga gaaccaccac 300
 ctacgaggac ggcggcatcc tgaccgccc ccaggacacc agcctggagg gcaactgcct 360
 gatctacaag gtgaaggtgc tgggcaccaa cttccccgcc gacggccccg tgatgaagaa 420
 caagagcggc ggctggggagc ccagcaccga ggtggtgtac cccgagaacg gcgtgctgtg 480
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 cagctaccgg agcaagaagg ccgtgcgggc cctgaccatg cccggcttcc acttcaccga 600
 catccggctg cagatgctgc ggaaggagaa ggacgagtag ttcgagctgt acgaggccag 660
 cgtggccccg tacagcgacc tgcccagaaa ggccaacaga tctcccggga tggtagcgcg 720
 cctgctgaag gagagcatgc gcatcaagat gtacatggag ggcaccgtga acggccacta 780
 cttcaagtgc gagggcgagg gcgacggcaa ccccttcgcc ggcaccacaga gcatgcggat 840
 ccacgtgacc gagggcgccc ccctgccctt cgccttcgac atcctggccc cctgctgcga 900
 gtacggcagc aggaccttcg tgcaccacac cgccgagatc cccgacttct tcaagcagag 960
 cttccccgag ggcttcacct gggagagaac caccacctac gaggacggcg gcatcctgac 1020
 cgcccaccag gacaccagcc tggagggcaa ctgcctgac tacaaggtga aggtgctggg 1080
 caccaacttc ccgcgcgacg gcccctgat gaagaacaag agcggcggct gggagcccag 1140
 caccgaggtg gtgtaccccg agaacggcgt gctgtgcggc cggaacgtga tggccctgaa 1200
 ggtgggcgac cggcggctga tctgccacca ctacaccagc taccggagca agaaggccgt 1260
 gcgggccctg accatgcccg gcttccactt caccgacatc cggtgcaga tgctgcggaa 1320
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 cgagaaggcc aactga 1396

<210> 16
 <211> 460
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 16
 Met Val Ser Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met
 1 5 10 15
 Glu Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp
 20 25 30
 Gly Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu
 35 40 45
 Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
 50 55 60
 Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
 65 70 75 80

Phe	Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr
				85					90					95	
Tyr	Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu
			100					105					110		
Gly	Asn	Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro
		115					120					125			
Ala	Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser
	130					135					140				
Thr	Glu	Val	Val	Tyr	Pro	Glu	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val
145					150					155					160
Met	Ala	Leu	Lys	Val	Gly	Asp	Arg	Arg	Leu	Ile	Cys	His	His	Tyr	Thr
				165					170					175	
Ser	Tyr	Arg	Ser	Lys	Lys	Ala	Val	Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe
			180					185					190		
His	Phe	Thr	Asp	Ile	Arg	Leu	Gln	Met	Leu	Arg	Lys	Glu	Lys	Asp	Glu
		195					200					205			
Tyr	Phe	Glu	Leu	Tyr	Glu	Ala	Ser	Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro
	210					215						220			
Glu	Lys	Ala	Asn	Arg	Ser	Pro	Gly	Met	Val	Ser	Gly	Leu	Leu	Lys	Glu
225					230					235					240
Ser	Met	Arg	Ile	Lys	Met	Tyr	Met	Glu	Gly	Thr	Val	Asn	Gly	His	Tyr
				245					250					255	
Phe	Lys	Cys	Glu	Gly	Glu	Gly	Asp	Gly	Asn	Pro	Phe	Ala	Gly	Thr	Gln
			260					265					270		
Ser	Met	Arg	Ile	His	Val	Thr	Glu	Gly	Ala	Pro	Leu	Pro	Phe	Ala	Phe
		275					280					285			
Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu	Tyr	Gly	Ser	Arg	Thr	Phe	Val	His
	290					295					300				
His	Thr	Ala	Glu	Ile	Pro	Asp	Phe	Phe	Lys	Gln	Ser	Phe	Pro	Glu	Gly
305					310					315					320
Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr	Glu	Asp	Gly	Gly	Ile	Leu	Thr
				325					330					335	
Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly	Asn	Cys	Leu	Ile	Tyr	Lys	Val
			340					345					350		
Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Asn
		355					360					365			
Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser	Thr	Glu	Val	Val	Tyr	Pro	Glu	Asn
		370				375					380				
Gly	Val	Leu	Cys	Gly	Arg	Asn	Val	Met	Ala	Leu	Lys	Val	Gly	Asp	Arg
385					390					395					400
Arg	Leu	Ile	Cys	His	His	Tyr	Thr	Ser	Tyr	Arg	Ser	Lys	Lys	Ala	Val
				405					410					415	
Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe	His	Phe	Thr	Asp	Ile	Arg	Leu	Gln
			420					425					430		
Met	Leu	Arg	Lys	Glu	Lys	Asp	Glu	Tyr	Phe	Glu	Leu	Tyr	Glu	Ala	Ser
		435				440						445			
Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro	Glu	Lys	Ala	Asn				
	450					455					460				

<210> 17
 <211> 1424
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 17
 accggtcgcc accatggtga ggggctgct gaaggagagc atgcgcatca agatgtacat 60
 ggagggcacc gtgaacggcc actacttcaa gtgcgagggc gagggcgacg gcaacccctt 120

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cgccggcacc cagagcatgc ggatccacgt gaccgagggc gccccctgc ccttcgcctt 180
cgacatccctg gccccctgct gcgagtagcg cagcaggacc ttcgtgcacc acaccgccga 240
gatccccgac ttcttcaagc agagcttccc cgagggttc acctgggaga gaaccaccac 300
ctacgaggac ggcggcatcc tgaccgcca ccaggacacc agcctggagg gcaactgcct 360
gatctacaag gtgaaggtgc tgggcaccaa cttccccgcc gacggccccg tgatgaagaa 420
caagagcggc ggctgggagc ccagcaccga ggtggtgtac cccgagaacg gcgtgctgtg 480
cggccggaac gtgatggccc tgaaggtggg cgaccggcgg ctgatctgcc accactacac 540
cagctaccgg agcaagaagg ccgtgcgggc cctgaccatg cccggcttcc acttcaccga 600
catccggctg cagatgctgc ggaaggagaa ggacgagtag ttcgagctgt acgaggccag 660
cgtggcccgg tacagcgacc tgcccagaaa ggccaacaga tctcccggga tggtagcggg 720
cctgctgaag gagagcatgc gcatcaagat gtacatggag ggcaccgtga acggccacta 780
cttcaagtgc gagggcgagg gcgacggcaa ccccttcgcc ggcaccaga gcatgcggat 840
ccacgtgacc gagggcgccc ccctgccctt cgcttcgac atcctggccc cctgctgcga 900
gtacggcagc aggaccttcg tgcaccacac cgccgagatc cccgacttct tcaagcagag 960
cttccccgag ggcttcacct gggagagaa caccacctac gaggacggcg gcatcctgac 1020
cgccccaccag gacaccagcc tggagggcaa ctgcctgatc tacaaggtga aggtgctggg 1080
caccaacttc cccgccgacg gccccgtgat gaagaacaag agcggcggct gggagcccag 1140
caccgaggtg gtgtaccccg agaacggcgt gctgtgcggc cggaacgtga tggccctgaa 1200
ggtgggcgac cggcggctga tctgccacca ctacaccagc taccggagca agaaggccgt 1260
gcgggcccctg accatgcccg gcttccactt caccgacatc cggctgcaga tgctgcggaa 1320
ggagaaggac gagtacttcg agctgtacga ggccagcgtg gcccggtaca gcgacctgcc 1380
cgagaaggcc aacagaactc gagctatgga tgatgatatc gccg 1424

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<210> 18
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion construct

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<400> 18
Met Val Ser Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met
  1          5          10          15
Glu Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp
          20          25          30
Gly Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu
          35          40          45
Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
          50          55          60
Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
          65          70          75          80
Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr
          85          90          95
Tyr Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu
          100          105          110
Gly Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro
          115          120          125
Ala Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser
          130          135          140
Thr Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val
          145          150          155          160
Met Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr
          165          170          175
Ser Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe
          180          185          190
His Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu
          195          200          205
Tyr Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro
          210          215          220
Glu Lys Ala Asn Arg Ser Pro Gly Met Val Ser Gly Leu Leu Lys Glu

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225		230		235		240
Ser Met Arg Ile Lys Met Tyr Met Glu Gly Thr Val Asn Gly His Tyr						
	245		250		255	
Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn Pro Phe Ala Gly Thr Gln						
	260		265		270	
Ser Met Arg Ile His Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Phe						
	275		280		285	
Asp Ile Leu Ala Pro Cys Cys Glu Tyr Gly Ser Arg Thr Phe Val His						
	290		295		300	
His Thr Ala Glu Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu Gly						
	305		310		315	320
Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly Ile Leu Thr						
	325		330		335	
Ala His Gln Asp Thr Ser Leu Glu Gly Asn Cys Leu Ile Tyr Lys Val						
	340		345		350	
Lys Val Leu Gly Thr Asn Phe Pro Ala Asp Gly Pro Val Met Lys Asn						
	355		360		365	
Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu Val Val Tyr Pro Glu Asn						
	370		375		380	
Gly Val Leu Cys Gly Arg Asn Val Met Ala Leu Lys Val Gly Asp Arg						
	385		390		395	400
Arg Leu Ile Cys His His Tyr Thr Ser Tyr Arg Ser Lys Lys Ala Val						
	405		410		415	
Arg Ala Leu Thr Met Pro Gly Phe His Phe Thr Asp Ile Arg Leu Gln						
	420		425		430	
Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe Glu Leu Tyr Glu Ala Ser						
	435		440		445	
Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys Ala Asn Arg Thr Arg Ala						
	450		455		460	
Met Asp Asp Asp Ile Ala						
	465		470			

<210> 19
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 19
 acatggatcc gctggtttgt tgaaaga

27

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 20
 acctcagtgc ttggctccca t

21

<210> 21
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> primer

<400> 21

atgggagcca agcactgagg t

21

<210> 22

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 22

tgacaagctt ctggtgtcac tgggaacaat ca

32

<210> 23

<211> 684

<212> DNA

<213> heteractis crispa

<400> 23

atggctggtt tgttgaaaga aagtatgcgc atcaagatgt acatggaagg cacggttaat 60
ggccattatt tcaagtgtga aggagagggga gacggcaacc catttacagg tacgcagagc 120
atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat tttggcaccg 180
tgttgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
attcttactg ctcatcagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaacaaatc aggaggatgg 420
gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
gcccttaaag tcggtgatcg tcgtttgatc tgccatctct atacttctta caggtccaag 540
aaagcagtcg gtgccttgac aatgccagga ttccatttta cagacatccg ccttcagatg 600
ccgaggaaaa agaaagacga gtactttgaa ctgtacgaag catctgtggc taggtacagt 660
gatcttctcg aaaaagcaaa ttga 684

<210> 24

<211> 227

<212> PRT

<213> heteractis crispa

<400> 24

Met	Ala	Gly	Leu	Leu	Lys	Glu	Ser	Met	Arg	Ile	Lys	Met	Tyr	Met	Glu
1				5					10					15	
Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Lys	Cys	Glu	Gly	Glu	Gly	Asp	Gly
			20					25					30		
Asn	Pro	Phe	Thr	Gly	Thr	Gln	Ser	Met	Arg	Ile	His	Val	Thr	Glu	Gly
		35					40					45			
Ala	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu	Tyr
	50					55					60				
Gly	Ser	Arg	Thr	Phe	Val	His	His	Thr	Ala	Glu	Ile	Pro	Asp	Phe	Phe
65					70				75					80	
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr
			85						90					95	
Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly
			100					105					110		
Asn	Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro	Ala
		115					120					125			
Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser	Thr
	130					135					140				
Glu	Val	Val	Tyr	Pro	Glu	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val	Met
145					150					155					160

Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Lys Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

<210> 25
 <211> 680
 <212> DNA
 <213> heteractis crispa

<400> 25
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 cattattttca agtgtgaagg agagggagac ggcaaccat ttgcaggtagc gcagagcatg 120
 aggattcatg tcaccgaagg ggctccatta ccatttgctt tcgacatttt ggcaccgtgt 180
 tgtgcgtacg gcagcaggac ctttgtccac catacggcag agattcccga tttcttcaag 240
 cagtcctttcc ctgaaggctt tacttgggaa agaaccacaa cctatgaaga tggaggcatt 300
 cttactgtctc atcaggacac aagcctggag gggaactgcc ttatatacaa ggtgaaagtc 360
 cttggtacca attttcctgc tgatggcccc gtgatgaaga aaaatcagga ggatgggagc 420
 caagcactga ggtggtttat ccagagaatg gtgtcctgtg tggacgtaat gtgatggccc 480
 ttaaagtcgg tgatcgtcgt ttgatctgcc atcactatac ttcttacagg tccaagaaag 540
 cagtcctgtgc cttgacaatg ccaggatttc attttacaga catccgcctt cagatgctga 600
 ggaaaaagaa agacgagtagc tttgaactgt acgaagcatc tgtggctagg tacagtgatc 660
 ttcttgaaaa agcaaattga 680

<210> 26
 <211> 226
 <212> PRT
 <213> heteractis crispa

<400> 26
 Ser Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met Glu Gly
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 Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn
 20 25 30
 Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly Ala
 35 40 45
 Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Ala Tyr Gly
 50 55 60
 Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe Lys
 65 70 75 80
 Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95
 Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly Asn
 100 105 110
 Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala Asp
 115 120 125
 Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu
 130 135 140
 Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met Ala
 145 150 155 160
 Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser Tyr
 165 170 175
 Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His Phe
 180 185 190

Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Lys Lys Asp Glu Tyr Phe
 195 200 205
 Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys
 210 215 220
 Ala Asn
 225

<210> 27
 <211> 910
 <212> DNA
 <213> heteractis crispa

<400> 27
 accatttgct ttggttcctt ggcaaacgaa agtttagaac gaaaactgac ccaaattaca 60
 tcttctctct ggatccttac catggctggt ttgttgaaaag aaagtatgcg catcaagatg 120
 tacatggaag gcacggttaa tggccattat ttcaagtgtg aaggagaggg agacggcaac 180
 ccattttacag gtacgcagag catgaggatt catgtcaccg aaggggctcc attaccattt 240
 gccttcgaca ttttggcacc gtgttgtgag tacggcagca ggacctttgt ccaccatacg 300
 gcagagattc ccgatttctt caagcagtct ttccctgaag gctttacttg ggaaagaacc 360
 acaacctatg aagatggagg cattcttact gtcctcagg acacaagcct ggaggggaac 420
 tgccttatat acaaggtgaa agtccttggg accaattttc ctgctgatgg ccccgatgag 480
 aagaacaaat caggaggatg ggagccatgc actgaggtgg tttatccaga gaatggtgtc 540
 ctgtgtggac gtaatgtgat ggcccttaaa gtcggtgatc gtcgtttgat ctgccatctc 600
 tatacttctt acaggtccaa gaaagcagtc cgtgccttga caatgccagg atttcatttt 660
 acagacatcc gccttcagat gccgaggaaa acgaaagacg agtactttga actgtacgaa 720
 gcatctgtgg ctaggtagag tgatcttctt gaaaaagcaa attgattgtt cccagtgcac 780
 ccagactgct gtcagctttt gggttaaagcc cgaaagacaa aaggacattt gtagtttagt 840
 ttatatattc ctttcatttg tgaatcaaca ttgtactctc tgtaaaccct taaaatgctc 900
 cattaaacct 910

<210> 28
 <211> 227
 <212> PRT
 <213> heteractis crispa

<400> 28
 Met Ala Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met Glu
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 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
 20 25 30
 Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Cys Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190

Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

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